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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.	OM nucleic - nucleic search, using sw model  Run on: June 24, 1999, 00:40:12; Search time 366.45 Seconds  (without alignments)	87.864 Million cell'updates/sec S-09-205-015-1	Scoring table: IDENTITY_NUC C Searched: 808301 segs, 1788773984 residues	GenEmbl:*  1: gb_bal:* 2: gb_ba2:* 3: gb_ba2:*	4: 9D_om:* 5: 9D_ov:* 6: 9D_pat:* 7: 9D_ph:*	12:* pr1:* pr2:* pr3:*	14: 95_5t.* 15: 95_8y.* 16: 95_un.* 17: 95_vi.* 17: 95_vi.* 18: 95_htg:*	* *	26: em_ov:* 27: em_pat:* 28: em_ph:* 30: em_pl:*	sy:* un:* vi:* htg:* sts:* sts:*	p11:* p12:* pr1:* pr3:* sts:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Result Query Description Some Some Some Social Description Score Match Length DB ID Description C

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Submitted (03-MAR-1997) to the DDBJ/EMBL/GenBank databases. Naotake Gusmitted (03-MAR-1997) to the DDBJ/EMBL/GenBank databases. Naotake Ogasawara, Nara Institute of Science and Technology, Graduate School of Blological Sciences; 8916-5 Takayama-cho, Ikoma, Nara 630-01, Japan (E-mail:nogasawa@bs.aist-nara.ac.jp, Tel:07437-2-5430, Fax:07437-2-5439)
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                                                                                                                                                                                                                                                                                                  Kashbara,Y., Nakai,S., Lee,S., Sadaie,Y. and Ogasawara,N. A 148 kbp sequence of the region between 35 and 47 degree of the Bacillus subtility genome Unpublished (1997) 3 (bases 1 to 148068)
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13901. .13912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FNYMVIVSRMSNMVQQPPTGHLIDDAGKNALAIVGEQFRFLIFGSTVGTILGIILLPS
FVALFSRAIIHLAGGGGSVFQVFRKGFSKQCFKNALSYLRLPSISYVKGFHMRLIPKR
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RESPONSIVE REGULATOR."
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RBS

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SYDLFAEK TREPYTTSPY I EGNLEPKREQLYTCAQY INNAKRP ILLAGGOMKAKA
RELLEFADKAAAP I VYLLPAGVYPDKHPHFLGNLGGIGTKPAY EAMEECDLLIMLGS
SEPYRDYLPDDTPATOLULSDPAK IGRRY PYTAGLYCDSALGIERLTEY I ERKEDREFL
NACTEHMQHWNE I ERDETRATTPLKPQQVYARLQERAADDAYLSVDYGTVYWMARH
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                                                                                                                                        SYNTHASE.
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ARGNOYVULKFLAQFFKLKRKRIIFDLFYFFFTYFLFFFGVIMSNAIFVVNLFYDLHL
SVGFLAMILWILAFFLEWTEVMITLSIEKTEMNKONFFIVFLMYFTYSQAMIVLVIYS
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16888. .19015
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16895. .19015
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                                                                                                                                                                                                                                                                                                                    'note-"FUNCTION UNKNOWN."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /hote="PROBABLE REGULATORY COMPONENT OF SENSORY TRANSDUCTION SYSTEM."
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                                         TERMINATOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B. SUBILLIS ATP-BINDING CASSETTE
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37739. 37745
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ATTITRITICALKONSOSYTIS GEOPHOFE EKAMBAVGAIVED EFFYTATITRITUCKENLKHF
ANNHKRIADERLDENSTENSTIS GEOPHOFE EKAMBAVGAIVED FEFTANGENIKHF
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EERLEABEELDESVEVOEHTRUNGELLAAGTSGGIGVIISAVFALISAVARALEELDESVEVENDELDESVEVENDELDESVEVENDELDESVEVENDELDESVEVENDELDESVEVENDELDESVEVENDELDESVEVENDELDESVEVENDELDESVEVENDELDESVEVENDELDESVERSTERVERDENDEREEGALFILEPDILFERNEN INTERPRESVERSESTERFORMERE KKLPHULRTFTPPRIJERENCRRIBERSVERSVESKENSTERSVERSEGALFILEPDILFERPRANCKESVERSTERSVERSELTIFPLOIFFORMYLESVERSTERSVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLLESVERSTERFORMYLESVERSTERFORMYLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESVERSTERFORMYLLESV
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TIDPPOPSYLALIANITARAY REALIZE TRAIT IN THE YRGINGHOTHEESELKOVKS ITN
TIDPPOPSYLALIANITARAY REALIZE TRAIT IN THE YRGINGHOTHEESELKOVKS ITN
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                   gene
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                                                        terminator
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78250. .78257
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EWVTAMSIGSPEHSYQAGGYNLFSISELTKPFQASAHLVGMTYLPSFAEYRANTISDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EIAESANRYVKHITNIELNPKVRLQRYLKQLESVDLT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107894.
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COMPLEMENT(LIZEZSS. .120302)

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120944. .122185

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complement(120298. .120305)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="PROBABLE REGULATORY COMPONENT OF SENSORY /Codon_start=1 /transl_table=11
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complement(119005. .119011)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TERMINATOR"
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IKRQFSDVEEVLIHVNPFFEE"
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131559. .131761
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                                                                                                          'note-"FUNCTION UNKNOWN, SIMILAR PRODUCT IN SYNECHOCYSTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="SIMILAR TO PENTACHLOROPHENOL-INDUCED PERIPLASMIC PROTEIN IN FLAVOBACTERIUM SP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131775. .131804
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LANDAIPVRAVLIVOETGENYTLIVOHYNYTATLITVOHTGOSTAVLIDISDR
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GTRTDYANWLLDVFDNLGIEKSHMIGLSLGGLHTMNFLLRMPERVKSAAILSPAETFL
BERHDFY KALGLTASNGVEFFLNWMINDQNVLHPIFYKQFRAVMODGSRRPNPNA
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SMEQPTYVNERVMRFVARFTALETSR"
COMPLEMENT (126432. .126437)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref-"PID:g1881352"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGPVVTAAGLIMIFVFAGFIFAGEASIKANGLALSFGVLFDAFIVRMTLIPSVHKIMG
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125424. .125456
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complement(128221. .128229)
/gene="yoft"
complement(128327. .129233)
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MULTIDRUG-EFFLUX TRANSPORTER REGULATORS IN B.SUBTILIS."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="FUNCTION UNKNOWN, SIMILAR PRODUCT IN E.COLI."
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TRANSPORT-ASSOCIATED PROTEIN ACTII IN STREPTOMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="PROBABLE RHO-INDEPENDENT TRANSCRIPTIONAL
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complement(126625. .127314)
/gene="ydfk"
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136797 137158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="PROBABLE RHO-INDEPENDENT TRANSCRIPTIONAL TERMINATOR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"FUNCTION UNKNOWN, SIMILAR PRODUCT IN SYNECHOCYSTIS."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(137954. .139597)
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                                                                                                                (YDGA_BACSU
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                                                                                                                                                                                                                                                                                                                                      'note-"SIMILAR TO YDFS GENE PRODUCT OF THIS ENTRY
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    'note" SIMILAR TO THIOREDOXIN."
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LLFFATWHTIFHVLMIIGFLLVLLIALRETLPERRIPSSIGTSVKTMGSLLKDRS
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REQUIRED FOR SURVIVAL IN MACROPHAGE."
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VLGKLSFWTPNDKGYKELDQARNELKKIKELDHQDKKD
COMPLEMENT (139604. .139613)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / John Damage Inducible DINB PROTEIN, SIMILAR PRODUCT IN SYNECHOCYSTIS."

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="PROBABLE AMINO ACID TRANSPORT PERMIASE."
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complement(139917. .141293)
/gene-"ydgr"
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/gene="dinB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(141993. .142000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142587. .14524
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/gene="ydgh"
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142138. .142143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
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DRELGRAFLVSNNYRTLLHWNKSNYFAVSIGMFADRIEQRVK
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NRKWMSRVLDGSYNERELGSG)"
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VSWCDFARAIFDEAVSQNMLEKAPLVNAIITADYPTPAKRPANSCLDLTKIQQAFGIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fawldtgtheslhegasfvrtvesvoglovacleeiawrngwltseovetlarpwykn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rhamnosyltrasferase; glycosyltransferase; exonuclease III; galactosyltransferase; hac transport protein; datop-4-keto-6-decoxy-D-glucose-3,5-epimerase; dTDP-4-rhamnose reductase; glucose-1,-posphate-thymidylyltransferas e; dTDP-D-glucose-4,6-dehydratase; lytic transglycosylase. Actinobacillus actinomycetemcomitans (strain:Y4) DNA. Actinobacillus actinomycetemcomitans subdivision; Pasteurellaceae; Actinobacillus, proteobacteria; gamma subdivision; Pasteurellaceae; Actinobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yoshida,Y., Nakano,Y., Yamashita,Y. and Koga,T.
Identification of a genetic locus essential for serotype b-specific antigen synthesis in Actinobacilius actinomycetemcomitans
Infect. Immun. 66 (1), 107-114 (1998)
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Direct Submission
Submitted (07-APR-1997) to the DDBJ/EMBL/GenBank databases. Yasuo
Submitted (07-APR-1997) to the DDBJ/EMBL/GenBank databases. Yasuo
Submitted (07-APR-1997) to the DDBJ/EMBL/GenBank databases. Yasuo
Yoshida, Kyushu University Faculty of Dentistry, Department of
Preventive Dentistry; 3-1-1 Maidashi, Higashi-ku, Fukuoka, Fukuoka
812-82, Japan (E-mail:yasuodha@mbox.nc.kyushu-u.ac.jp,
Tel:092-642-6423, Fax:092-642-6354)
Location/Qualifiers
1. 24907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinobacillus actinomycetemcomitans DNA for glycosyltransferase, lytic transglycosylase, dTDP-4-rhamnose reductase, complete cds.
                                                                                                               Gaps
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          DB 1; Le
3.4e+03;
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          9;
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9; .Conservative
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Query Match
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                                                                                                                                                                                                                 LCVTVKENMUVILLEPFISKRREIRHGSMYSIFIIISILMIVLAMKLTEAGSHFKE
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PIMLIFSSFILKKSEKTSNNKTISKYFIIVPFLFFISSFITINTLVSRYYMG"
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SNSFAXTRRSVPEELGGFPDMYILAEDMYITARMYLAGTKVAYCABATVFHSHYTLS
GELQRYFDTGVFQQEGGWIQQTFGKWASEGKKFVLSELKFLVKNAPHLLPKALLSTFA
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SLOGIPLYGAEISHFFSSETIVLRIPNKĻAKRSTRLMKRTFDIVVSSLLILLLAPLFL
                                                                                                                                                                  PVLLILSLPMTMFQMGSTNPDSIIFSLSVFIGSLLARGLDSNYNFTHKDFCKLLFSIF
                                                                                                     antnvyfpliylpqalgsflgstldlslynmyylakiftllvsiailyfasvqyrlsi
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13072. .14043
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8072. . 9139
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IDYIRBENYKVPPQAARNFKINASYILAYPHINNLSRKAAKYYFDIFKQTRSLKQLIIA
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NYPTTFAFLRANVGAATYAYPYKSYFAGTVAYLIKKSAARTFLAILEQEKPFWLADDF
LLFETQFKLNNNVVRPLAVIENPQLVSNLEAVRGSKSNNLAKKLLKYPLKKLLAVKKN
Direct Submission
Submitted (07-APR-1997) to the DDBJ/EMBL/GenBank databases. Yasuo Yoshida, Kyushu University Faculty of Dentistry, Department of Parally Dentistry; 3-1-1 Maldashi, Hiqashi ku, Fukuoka, Fukuoka 812-82, Japan (E-mail:yasuodha@mbox.nc.kyushu-u.ac.jp, Tel:092-642-6423, Fax:092-642-6354)
Tel:092-642-6423, Fax:092-642-6354)
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24126. .24668
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Yoshida,Y., Nakano,Y., Yamashita,Y. and Koga,T.
Identification of a genetic locus essential for serotype b-specific
antigen synthesis in Actinobacillus actinomycetemcomitans
Infect. Immun. 66 (1), 107-114 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MQFLITGGAGFIGSALIRWLIQHTEHDIINVDKLTYAGNLCALY
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Actinobacillus.
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Yoshida, Y.
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1 4293 c 5099 g 7976 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (18-APR-1997) to the DDBJ/EMBL/GenBank databases.
Ken-ichi Kasuya, The Institute of Physical and Chemical Research (RIKEN), Polymer Chemistry Lab.; Hirosawa 2-1, Wako, Saitama 351-01, Japan (E-mail:kkasuya@postman.riken.go.jp, Iel:048-462-1111, Fax:048-462-4667)
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100.0%; Score 9; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 9; Conservative 0; Mismatches 0;
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11arity 100.0%; Pred. No. 4.5e+03;
Conservative 0; Mismatches 0;
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119. .1603
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RESULT' 5 AB008139/c LOCUS

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ACCESSION

JOURNAL REFERENCE AUTHORS

JOURNAL

FEATURES

AUTHORS TITLE

REFERENCE

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Harada, H.

Direct Submission
Submitted (15-OCT-1997) to the DDBJ/EMBL/GenBank databases. Hosami
Harada, Graduate School of Science, University of Tokyo, Department
of Balogical Sciences; Hongo, Bunkyo-ku, Tokyo 113, Japan (B-mail:hosami@biol.s.u-tokyo.ac.jp,
Bunkyo-ku, Tokyo 113, Japan (B-mail:hosami@biol.s.u-tokyo.ac.jp,
Tel:03-3812-2111, Fax:03-3816-1965)

Location/Qualifiers
e
//organism="Erwinia aphidicola"
//strain="IAM14479"
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Hardân,H. and Ishikawa,H.
Phylogenetical relationship based on groE genes among
phylogenetical related Enterobacter, Pantoea, Klebsiella, Serratia,
phenotypically related Enterobacter, Pantoea, Klebsiella, Serratia,
and Erwinia species
J. Gen. Appl. Microbiol. 43, 355-361 (1997)
(bases 1 to 1950)
                                                                                                                                                                           DNA BCT 21-MAR-1998 for GroES protein homologue, GroEL protein
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Erwinia aphidicola (strain:IAM14479) DNA.
Erwinia aphidicola
Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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1larity 100.0%; Pred. No. 6.4e+03;
Conservative 0; Mismatches 0;
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Erwinia aphidicola gene
homologue, partial cds.
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Matches 9; Conserv
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harada, H. and Ishikawa, H.
Phylogenetical relationship based on groE genes among
Phylogenetical related Enterobacter, Pantoea, Klebsiella, Serratia,
and Erwinia species
J. Gen. Appl. Microbiol. 43, 355-361 (1997)
2 (bases 1 to 1933)
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Briterobacter gergoviae (strain:JCM 1234) DNA.

Enterobacter gergoviae

Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Enterobacter gergoviae gene for GroES protein homologue, GroEL
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                      mannosyltransferase; ATP binding component of ABC-transporter;
phosphomannomutase; GDP-mannose pyrophosphorylase;
gluconate-6-phosphate dehydrogenase; integral membrane component of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (07-JAN-1998) to the DDBJ/EMBL/GenBank databases.
TSuyoshi Sugiyama, Alchi Medical University, Department of
Microbiology and Immunology; Yazako, Nagakute, Alchi 480-11, Japan
(E-mail:sugiyama@aichi-med-u.ac.jp, Tel:0561-62-3311,
                                                                                                                                                                                                                                                             ABC-transporter. Set ann: F492) DNA, clone_lib:31 clone:pTSO8. Escherichia coli (Strain: F492) DNA, clone_lib:31 clone:pTSO8. Escherichia coli Eubacteria: proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sugiyama,T., Kido,N., Kato,Y., Kolde,N., Yoshida,T. and Yokochi,T. Generation of escherichia coli O9a serotype, a subtype of E. coli O9, by transfer of the wb* gene cluster of klebsiella O3 into E. coli via recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sugiyama,T., Kido,N., Koide,N., Kato,Y., Yoshida,T., Jiang,G., Paeng,N., Takahashi,K., Morikawa,A. and Yokochi,T.
Nucleotide sequence of Escherichia coli O8 wb gene cluster
Unpublished (1998)
3 (bases 1 to 15295)
                                                                       21-MAY-1998
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Escherichia coli O8 wb gene cluster, complete cds.
AB010150
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7gene-70RR425.

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7gene-70RE469.
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IFAPYLHGGFWLFRSKALLELGGFDBRFFWYMEDVDLSRRCAEKFGNIYYPLAQVIHL
HEQGSYKNKTLLKAHLKSAWQYFCKWGWLYDAQRSSLNGKCLKQRNG"
COMPLOMENT (1116. 2545)
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/translation="MVIASIVIYKHSYSDLKQTLDSLLAVSSINKIVLVDNDHSDWAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (06-SEP-1994) M. Stark, Tel Aviv University, Dept of
Molecular Microbiology & Biotechnology, Ramat-Aviv, 69978 Tel-Aviv,
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LFALKNLDCADPLLICNEEHRFLAAEQMREIGISAKIILEPEGKNTAPAITLAALYQI
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Eubacteria; proteobacteria; gamma subdivision; Moraxellaceae;
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                                                                                                                                                                                              Length 15295;
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1. .2748
/organism="Acinetobacter calcoaceticus"
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                                                                                                                                                                                         100.0%; Score 9; DB 1; Le
100.0%; Pred. No. 4.8e+03;
ive 0; Mismatches 0;
                                                                        /note="putative bi-functional"
3701 c 4063 g 3924 t
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/db_xref="taxon:471"
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291. .1088
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/transl_table=11
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11579. .11582
13886. .13906
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281. .1088
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1 (bases 1 to 2748)
Stark, M. and Kaplan, N.
Unpublished
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Best Local Similarity 100.
Matches 9; Conservative
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/db_xref="PiD:92983080"
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DLTDIYKEEDVNKEICDGILGGAAFLDKLMSGEYAVITL"
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LFGCLNCGVCTASCPSNRFFDYSPREIVQRFLENDIDVLYDWMHEYIWACSQCFTCWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative indicates no similarity to known proteins Hypothetical indicates similarity to a protein of unknown function. Location Qualifiers
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Deckert, G., Warren, P.V., Gaasterland, T., Young, W.G., Lenox, A.L.,
Graham, D. E., Overbeek, R., Snead, M.A., Keller, M., Aujay, M.,
Huber, W., Feldman, R.A., Short, J.M., Olson, G.J. and Swanson, R.V.
Direct Submission
Submitted (25-JUL-1997) Diversa Corporation, Genomics, San Diego,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eubacteria; Aquificales; Aquificaceae; Aquifex.

[ bases 1 to 14801)

Deckert,G., Warzen,P.V., Gaasterland,T., Young,W.G., Lenox,A.L.

Graham,D.E., Overbeek,R., Shorad,M.A., Keller,M., Aujay,M.,

Huber,R., Peldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V.

The complete genome of the hyperthermophilic bacterium Aquifex
                                           Gaps
                                                                                                                                                                                                                                                          AEU00688 14801 bp DNA BCT 30-OCT-1
Agulfax aeolicus section 20 of 109 of the complete genome.
92983063
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                                              Indels
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            Pred. No. 6.1e+03; 
; Mismatches 0;
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/organism="Aquifex aeolicus"
/strain="VF5"
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/db_xref="PID:92983070"
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335. .883
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/db_xref="PID:g2983069"
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903. .1328
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1455. .2207
/gene="aq_391"
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335. .883
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            100.08;
                                     9; Conservative
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Matches 9; Conserv
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AE000688/c
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AUTHORS
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SIQMHHHRSEHWIVVNGTAKIHKGKESFLLTENQSTYIPLGEIHALENPGKVPLELIE
VQSGSYLGEDDIVRFEDLYGRC"
complement(2541. .2545)
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/db_xref="Florests" | /db_xref="$38719"
/db_xref="$38719"
/db_xref="$4015S-PROT:P31004"
/db_xref="$4015S-PROT:P31004"
/db_xref="$4015S-PROT:P31004"
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VSAAWDTVTESRMAIAMAQNGGIGILHKNMDIAAQAAEVRRVKKFEAGMVKDPITVSP
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VGAAVGTGADTPSRVEALVEAGVDIVVDTAHGHSAGVIERVRWVKQNFPQVOYIGGN
IATGDAALALDAGADAVKOGIGPGSICTTRLYAGIGMPQISAIDSYASALKDDIPLI
ADGGIPFSGADRYAGIGPGSTIMVGSLLAGTEEAPGEVEFTQGRYKAYRGMGSLGAM
AGGIPFSGADRYROGISGATIMVGSLLAGTEEAPGEVEFTQGRYKAYRGMGSLGAM
IEDDLRQMAKFVKITSAGMSESHVHDVTITKEAPNYRVG"
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A calcoaceticus gene for inosin-5-monophosphate dehydrogenase and
putative feredoxin.
X66859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (11-JUN-1992) U. Anderegg, Univ. Leipzig, Fach.
Blowissenschaften, Talstrase 33, 0-7010 Leipzig, FRG
2 (bases 1 to 2878)
Anderegg, U., Schunck, W.H., Asperger, O. and Kleber, H.P.
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                                                                                                                                                                                                                                           DB 1; Length 2748;
6.2e+03;
hes 0; Indels
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    2878
    /organism-"Acinetobacter calcoaceticus"
/strain-"EB 104"

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/db_xref="PID:938720"
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                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                        Query Match 100.0%; Score 9;
Best Local Similarity 100.0%; Pred. No.
Matches 9; Conservative 0; Mismatch
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/clone="puc 119-64"
252. .617
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Acinetobacter calcoaceticus
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/codon_start=1
                                                                    /gene="epsM"
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1 (bases 1 to 2878)
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TITLE
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JOURNAL
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SPKE"
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Graham,D.E., Overbeek,R., Snead,M.A., Keller,M., Aujay,M.,
Huber,K., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deckert, G., Warren, P.V., Gaasterland, T., Young, W.G., Lenox, A.L. Graham, D.E., Overbeek, R., Snead, M.A., Keller, M., Aujay, M., Huber, R., Feldman, R.A., Short, J.M., Olson, G.J. and Swanson, R.V. The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                        30-OCT-1997
                                                                                                                                                                         AE000692 15304 bp DNA BCT 30-OCT-1
AE011fex aeolicus section 24 of 109 of the complete genome.
AE000692 AE000657
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Aquifex aeolicus
Eubacteriai, Aquificales; Aquificaceae; Aquifex.
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98196666
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complement(1101. .2336)
/gene="aq_478"
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KTKHKHLDAIVQYHPENSPGPHDSYLLFKEFVKMAQG"
3311 c 3301 g 3744 t
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COMPLEMENT (6532. .7167)
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Hypothetical indicates similarity to a protein of unknown function.
Lotation/Qualifiers
1. .14150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-JUL-1997) Diversa Corporation, Genomics, San Diego,
                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 14150)
Deckert,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox,A.L.,
Graham,D.B., Overbeek,R., Snead,M.A., Keller,M., Aujay,M.,
Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V.
Direct Submission
                                                     Aquifex aeolicus

Eubacteria; Aquificales; Aquificaceae; Aquifex.

I (bases 1 to 14150)

Deckert,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox,A.L.

Graham,D.E., Overbeek,R., Snead,M.A., Keller,M., Aujay,M.,

Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V.

The complete genome of the hyperthermophilic bacterium Aquifex
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                                                                                                                                                                                                                                                                              Nature 392 (6674), 353-358 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="neac"
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                                                       ORGANISM
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REFERENCE
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                                                                                                               REFERENCE
                                                                                                                                          AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                            TITLE
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KAKLIKECCEKLIELYKGEVPKSVGELVKLPGVGRKTANMVIGGAYNLPAIIVDRHVH
RVVERISLSKQKNPDKMEMELSEIVPQELWTKFSLLLINHGKTICKARNPECEKCPIL
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LIDLLVKAFEDFGDLEDVEGYVEDSGEGRWCYKESVELGAPIPVIAQSFYERFSSREK
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Aquifex aeolicus section 29 of 109 of the complete genome.
AE000697 AE000657
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                                                                                                                                                                                                                                                                                                                                      complement(12274. .13569)
/gene="gsdA"
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RLEELKELLKRRLRTGRR"
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                                                 TALALLIREAIDIILKDIDKVMEEIKRLAFEHKDTLMMGRTHGVHAEPYTFGLKMCVW
YDEMRRQKERLLFARENVLYGKISGAVGTYSNIPPEVEKLALEELGLKIEPASTQIVH
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              LKKIEEKTYVDKKVVEKIKEKEKVFKHDVLAFVSVIAEQVGEEGRYIHMGLTSSDVVD
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/codon -
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/gene="aq_600"
complement(12640. .13122)
/gene="aq_600"
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13479. .14015
/gene="aq_601"
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RVVAYSALHRRESRGGHSREDYPQRDDKNFLKHSLVYYDKNGNLKLEYIPVRITKYKP
EERKY"
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REAELLKEAQYAWNTGDFYRAHEILEEVWGLFKNEEIKKCYRGLIRAAIALHRFKEGN
PQSGANVVKQALLDMANCPDNFRGINLGEIRAYLEEVLGTKEIGNPPELKYNIKSEE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEEEQNKVEKLREYILKLDSCEICTRGLEGEEFFNCLTQNVDFLTATHIANFFFEEFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EAFRNNTPVIARDIKVFREIAGDNAFFFENTKNPEVIANAIKTWLELYRKGLHPKPAN
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5552. .7246
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VLEKAGVKPEEVSLVIPHQANVRIINALAEKLNIPKEKVFVNIQKYGNTSAASIPIAL
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                                                                                                                                                                                                                                                          complement(3522. .5288)
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EITEBGSPETVTQAYYKLMASLENKEGITFLOAKYGHRKAV KEVRILKSEHGYTNNEP
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MPLNLAPGKYTLIVALHKGMDHAQECYHWIDNVCNFEVNGFKRGGFVGYVYLFTEFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Putative indicates no similarity to known proteins Hypothetical indicates similarity to a protein of unknown function. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MMIRVFDVWKKYKYKKPODRLKEIIFRKPFHEELWVLKGINLE
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Deckert,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox,A.L.,
Graham,D.E., Overbeek,R., Snead,M.A., Keller,M., Aujay,M.,
Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (25-JUL-1997) Diversa Corporation, Genomics, San Diego
                                                                                                                                                                                                                                                                                                                     Lenox, A.L.,
                                                                                                                                                                                                                                                                                                     Deckert, G., Warren, P.V., Gaasterland, T., Young, W.G., Lenox, A.L. Graham, D.E., Overbeek, R., Snead, M.A., Keller, M., Aujay, M., Huber, R., Feldman, R.A., Short, J.M., Olson, G.J. and Swanson, R.V. The Complete genome of the hyperthermophilic bacterium Aquifex aeolicus
                                                 30-0CT-1997
Aquifex aeolicus section 55 of 109 of the complete genome. 92983569
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Aquifex aeolicus
Ebbacteria: Aquificales; Aquificaceae; Aquifex.
(bases 1 to 15467)

    11. .15467
    /organism="Aquifex aeolicus"
/strain="VF5"

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                                                                DEFINITION
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COMMENT

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IYRKLLKEKIVLGLPLDRFYEDLKKOFTATLIAVTEKRTFKEEIDSVLALL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="Producty of the control of
                                                                                                                                                                                      /translation-"WEDFYVEDYLVKGDRYYTKEHEWVRVKNGFAEVGITDYAQKQLG
DIVYVDLPEKGKEVDAGDTLANIESVKNVAPVYAPVTGTVVEVNEDLKDEPGIINDDP
YEAGWIAVIEMKDPTEVEDLMTAQDYAEYLKEIVEEEKEEEVEVKEEELIETESIEEL
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Sanith, D. R., Deloughery, C., Lee, H.-M.,
Dubois, J., Aldredge, T., Bashirzadeh, R., Blakely, D., Cook, R.,
Gilbert, K., Barrison, D., Hoang, L., Reagle, P., Lumm, W., Pothier, B.,
Qiu, D., Spadafora, R., Vicare, R., Wang, Y., Wierzbowski, J.,
Gibson, R., Jiwani, N., Caruso, A., Bush, D., Safer, H., Patuwell, D.,
Prabhakar, S., McDougall, S., Shimer, G., Goyal, A., Pietrovski, S.,
Church, G. M., Daniels, C. J., Mao, J.-i., Rice, P., Nolling, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanobacterium thermoautotrophicum
Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
Methanobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AE000796 16071 bp DNA BCT 13-NOV-1997 Methanobacterium thermoautotrophicum from bases 10151 to 26221 (section 2 of 148) of the complete genome.
4E000796 AE000666 g2621057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                 /product-"glycine cleavage system protein
/db_xref="PID:92983578"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanobacterium thermoautotrophicum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(14874. .15329)
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                                                                                 /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="gcsP2"
13569. .14888
/gene="gcsP2"
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AE000796/c
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative protein"
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/db_xref="putative protein"
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Enytylwgdelseeffytalsffsirodskeravyinnegdelkklogrkrerellir
Vlrnvksnyvflyydakloglesseplksyaskerlittdekkrekek
KGINVENDALEVLLOLGYRABELEVEKLIDFASEKRITTLDEWKRYRESNYN
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KAMESVGIKNNFLKKERSYLKADSLISFGIHPLOIMKILSSYALKLTILKEREKGEDLN
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PFTTDRLPDLIDLRILDENPDLYJCAEVAGPENPYIEESPPYWEDVOLFVFDFMKN
EGGFLSGOEKMELIEKYNLPHVEILGRFTASEEGIKKIKEILKRFNEEGREGVYKKED
SERNKRAKTITSYNLMADIKTNAKNMLQLPPEYYNRILLRLVLFWIEEGLKTTEHLYE
ELGRAFIDGLROAIEOFEKEHKYYKTFTCKFRKENAIALLELLSKTSKHIQVKERRE
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/db_xref-"PID:92983880"

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Itanslaid-maritolkeifkisdreksytlopkdykliptigelkkpyvvvvv

EITROKNGYKLRLSMSGYVELBCSRCIEVYEKDISOBKTKLLONIPHEEGTFHLKPKD

LEVTFMEEPDKVNIADLVREBIILSIPMKPLCSPQCRGIFGYAVELEEPEKETKKESS
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Product="bibosomal protein L32"
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LPNLNMRFVCKWVNLRVENERSAFTRKLEKGDVLRIPIAHHDGRYYVPEEELRKMEEN
GQILFRYCDEQGEVKEEVNPNGSVSNIAGVMNKEGNVFGMMPHPERASEDILGSHDGL
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FAEYGGIPLLGAKKPVIITHGRANAKAIKNAVRVAGEFLNTDFNKKLVYNLKTLIPEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(9377. .9901)
                                                                                                                                                                                          complement(9186. .9377)
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11008. .11691
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11008. .11691
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11684. .12787
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CDS

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2709. .4079
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LDEVYSKWGTGSGYGLIAACYPFFEALIFVLTGASPPLSAPSAPSGRTIGFLTIFTGG
SPDFQYYVLPVLALIAVFLVASSRRVEIPISMGGGKRLSRGAVGKYPLRFITATG
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IGWLGWYILCSFAMSQIFRKFMGLKGGM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MPVILTSALLLNVQLLANVEQKLGYPILGTVSNGQAYDGLAYLLTAPRSIDALILDPF
RVVFYAVVFIGLCVLFAMLWVEISNIGPRHVARQLYOMGMQIPGFRSSRGQFEKILKR
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/note="Function Code:4.01 - Nucleotide Metabolism, Purine
metabolism : similar to, sp:LN:KAD_METJA AC:P43409,
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/codon_start=1
/transl_table=11
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Ribosomal proteins; similar to, sp:LN:RL34_METJA
AC:P54053, p()=1.6E-28, pid=58%"
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4678. :5244
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Submitted (10-AUG-1997) Genomics and Technology Development, Genome
Therapuetics Corporation, 100 Beaver Street, Waltham, MA
02154-8448, USA
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1118. .1768
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98037514
                                                                                                                                                                                                               Location/Qualifiers
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                                                     2 (bases 1 to 16071)
Smith, D.R.
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MEDLINE
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                                                                                     AUTHORS
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gene

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RAQRISVRESKDIETVREEIRIRERSEAQRYREIHGIDVDDLEVYDIVINTNRFDAEA
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complement(7322. 7408)
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(tRNA-Ser-1 anticodon:99a); 100% ID to interval
968187-968101
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967976-968061"
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Ribosomal proteins; similar to, sp:LN:RS2_METJA AC:P54109,
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Matches 9; Conser
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RQKSYR'
10963. .11130
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NQIGTLTDTYLTYKLALENRYTPVVSHRSGETTDDTIAHLAVAFGAPLIKTGALGGER
IAKLNELIRIQEEIPYSRMADLPF"
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                                                                                                                                                                                                                                 (bases 1 to 10932)

Smith, D.R., Doucette-Stamm, L.A., Deloughery, C., Lee, H.-M.,
Dubols, J., Aldredge, T., Bashirzadeh, R., Blakely, D., Cook, R.,
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Church, G.M., Daniels, C.J., Mao, J.-i., Rice, P., Nolling, J. and
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                                                                                                                                              Methanobacterium thermoautotrophicum.
Methanobacterium thermoautotrophicum
Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
Methanobacterium.
             AE000801 10932 bp DNA BCT 13-NOV-1997 Methanobacterium thermoautotrophicum from bases 68653 to 79584 (section 7 of 148) of the complete genome.
42000801 AE000666 g2621145
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CDS

CDS

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CHARLES ALLOW-"MADELEGYFLILKRDGFIEKTIGYGADIPHGMGSFAGLMDHGSQ
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COMPLEMENT (10316 . 10404)

Anote="91" bp direct repeat includes part of MTH123
(sensory transduction histidine kinase - paralog.fam. 1);
81% ID to interval 74694

COMPLEMENT (10316 . 10398)

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(sensory transduction histidine kinase - paralog.fam. 1);
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9965. .9189
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complement(9788. .10858)
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complement(8368. .8943)
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5187. 5930
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COMPLEMENT(5559. .6975)
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//gene="MTH116"

5187. .5930

//gene="MTH116"

//note="Function Code:14.01 - Unknown, Conserved protein;

similar to, pir:LN:G64472 AC:G64472, p()=2.8E-22, pid=25%"

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Histidine metabolism; similar to, gp:GI:g1001367,
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                                                                                              4550. .5119
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/note="Punction Code:14.00 - Unknown, ; similar t
gp:gI:g1835286 LN:XCU70889, p()-0.99995, pid-09%"
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complement(5959..6975)

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                  gene
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CDS

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repeat_region complement(10316. .10368)

// note="53 bp direct repeat includes part of MTH123
// sensory transduction histidine Kinase - paralog.fam. 1);

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1267 TCTGAGTCA 1259

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